



SEQUENCE LISTING

<110> MacPhee, Colin Houston  
Tew, David Graham  
Southan, Christopher Donald  
Hickey, Deirdre Mary Bernadette  
Gloge, Israel Simon  
Lawrence, Geoffrey Mark Prouse  
Rice, Simon Quentyn John

<120> Lipoprotein Associated Phospholipase A2,  
Inhibitors Thereof and Use of the Same in Diagnosis and  
Therapy

<130> P30693C4X1C1

<140> 09/922,067  
<141> 2001-08-03

<150> 09/193,130  
<151> 2000-11-28

<150> 08/387,858  
<151> 1994-06-24

<150> PCT/GB94/01374  
<151> 1994-06-24

<150> GB 9313144.9  
<151> 1993-06-25

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1 5 10 15  
Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His  
20 25 30  
Lys Asp Phe Asp Gln  
35

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Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro  
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Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn  
20 25 30

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<212> PRT  
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1 5 10 15  
Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly  
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Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr  
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Pro Ala Asn

<210> 5

<211> 420

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> 265, 390, 395, 403, 406

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gtgttgattt gtttgtttaa tgggtgtccc tggataaga ttctcatcat ctccttcaat 120  
caaggcagtcc cactgatcaa aatctttatg aagtcctaaa tgctttgtaa agaatgctaa 180  
tgaagctttt ttgctaaagat caatagctgc atttgaatct atgtctccct ttaattttag 240  
catgtgtcca attatttgc cagtnngccaa agtgaagtca gcaaaattct ggtggactga 300  
acccctgatt gtaatcatct ttctttcttt atcagggttag tagcatttt tcatttttat 360  
gatatttagca ggatatttggaa aatattcagn gttgnntaaaa agngngngct gagggattct 420

<210> 6

<211> 379

<212> DNA

<213> Unknown

<220> Homo sapien

<221> misc\_feature

<222> 84

<223> n = A,T,C or G

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tgctaatatc ataaaaatga aaaaatgcta ctcacactgat aaagaaagaa agatgattac 60

aatcaggggt tcagtcacc agantttgc tgacttact tttgcaactg gaaaaataat 120  
tggacacatg ctcattaa agggagacat agattcaat gtagctattg atcttagcaa 180  
caaagcttca ttagcattct tacaaaagca tttaggactt cataaagatt ttgttcagtg 240  
ggactgctt attgaaggag atgatgagaa ttttattcca gggaccaaca ttaacacaac 300  
caattcaaca catcatgtt acagaacttc ttccagggaa taggagaaa tacaattggg 360  
gtttaaaata ggaaaaata 379

<210> 7

<211> 279

<212> DNA

<213> Unknown

<220> Homo sapien

<221> misc\_feature

<222> 257

<223> n = A,T,C or G

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gaagaatgca tttagattaa agtttgcata ggaacaactg aaggactcta ttgataggga 60  
aaaaatagca gtaattggac attctttgg tggagcaacg gtatattcaga ctcttagtga 120  
agatcagaga ttcagatgtg gtattgcctt ggatgcattt atgtttccac tgggtgatga 180  
agtatattcc agaattccctc agccctctt ttttatcaac tctgaatattt tccaatatcc 240  
tgctaatacataaaaaantgg aaaaatgcta ctcacctgg 279

<210> 8

<211> 572

<212> DNA

<213> Homo sapien

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aaaatagcag taattggaca ttcttttaggt ggagcaacgg ttattcagac tcttagtgaa 60  
gatcagagat tcagatgtgg tattgcctg gatgcatttga tggttccact ggggtgatgaa 120  
gtatattccca gaattccctca gcccctctt tttatcaact ctgaatattt ccaatatcc 180  
gctaataatca taaaatgaa aaaatgctac tcacatttgcata aagaaagaaaa gatgatttaca 240  
atcaggggtt cagtcacca gaaattttgtt gacttcactt ttgcacactgg caaaaataatt 300  
ggacacatgc tcaattaa gggagacata gattcaatg tagtatttgc tttagcaac 360  
aaagcttcat cagcattctt acaaaagcat ttaggacttc ataaagattt tgatcagtg 420  
gactgcttgc ttgaaggaga ttagtgcata aatcaacaca tcatgttaca gaaatcgata aatcaatataa ggtttaataat 480  
aatcaacaca tcatgttaca gaaatcgata aatcaatataa ggtttaataat 540  
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1 5

cat gtg ctt ttc tgc ctc tgc ggc tgc ctg gct gtg gtt tat cct ttt 103  
His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe  
10 15 20

gac tgg caa tac ata aat cct gtt gcc cat atg aaa tca tca gca tgg 151  
Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp  
25 30 35

gtc aac aaa ata caa gta ctg atg gct gct gca agc ttt ggc caa act 199  
Val Asn Lys Ile Gln Val Leu Met Ala Ala Ser Phe Gly Gln Thr  
40 45 50

aaa atc ccc cgg gga aat ggg cct tat tcc gtt ggt tgg aca gac tta 247  
Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu  
55 60 65 70

atg ttt gat cac act aat aag ggc acc ttc ttg cgt tta tat tat cca 295  
Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro  
75 80 85

tcc caa gat aat gat cgc ctt gac acc ctt tgg atc cca aat aaa gaa 343  
Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu  
90 95 100

tat ttt tgg ggt ctt agc aaa ttt ctt gga aca cac tgg ctt atg ggc 391

Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly Thr His Trp Leu Met Gly  
 105                        110                        115

aac att ttg agg tta ctc ttt ggt tca atg aca act cct gca aac tgg    439  
 Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr Pro Ala Asn Trp  
 120                        125                        130

aat tcc cct ctg agg cct ggt gaa aaa tat cca ctt gtt gtt ttt tct    487  
 Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser  
 135                        140                        145                        150

cat ggt ctt ggg gca ttc agg aca ctt tat tct gct att ggc att gac    535  
 His Gly Leu Gly Ala Phe Arg Thr Leu Tyr Ser Ala Ile Gly Ile Asp  
 155                        160                        165

ctg gca tct cat ggg ttt ata gtt gct gct gta gaa cac aga gat aga    583  
 Leu Ala Ser His Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg  
 170                        175                        180

tct gca tct gca act tac tat ttc aag gac caa tct gct gca gaa ata    631  
 Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp Gln Ser Ala Ala Glu Ile  
 185                        190                        195

ggg gac aag tct tgg ctc tac ctt aga acc ctg aaa caa gag gag gag    679  
 Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr Leu Lys Gln Glu Glu Glu  
 200                        205                        210

aca cat ata cga aat gag cag gta cgg caa aga gca aaa gaa tgt tcc    727  
 Thr His Ile Arg Asn Glu Gln Val Arg Gln Arg Ala Lys Glu Cys Ser  
 215                        220                        225                        230

caa gct ctc agt ctg att ctt gac att gat cat gga aag cca gtg aag    775  
 Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp His Gly Lys Pro Val Lys  
 235                        240                        245

aat gca tta gat tta aag ttt gat atg gaa caa ctg aag gac tct att    823  
 Asn Ala Leu Asp Leu Lys Phe Asp Met Glu Gln Leu Lys Asp Ser Ile  
 250                        255                        260

gat agg gaa aaa ata gca gta att gga cat tct ttt ggt gga gca acg    871

|   |     |     |      |
|---|-----|-----|------|
| Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr |     |     |      |
| 265   | 270 | 275 |      |
| gtt att cag act ctt agt gaa gat cag aga ttc aga tgt ggt att gcc |     |     | 919  |
| Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala |     |     |      |
| 280   | 285 | 290 |      |
| ctg gat gca tgg atg ttt cca ctg ggt gat gaa gta tat tcc aga att |     |     | 967  |
| Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile |     |     |      |
| 295   | 300 | 305 | 310  |
| cct cag ccc ctc ttt ttt atc aac tct gaa tat ttc caa tat cct gct |     |     | 1015 |
| Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala |     |     |      |
| 315   | 320 | 325 |      |
| aat atc ata aaa atg aaa aaa tgc tac tca cct gat aaa gaa aga aag |     |     | 1063 |
| Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser Pro Asp Lys Glu Arg Lys |     |     |      |
| 330   | 335 | 340 |      |
| atg att aca atc agg ggt tca gtc cac cac aat ttt gct gac ttc act |     |     | 1111 |
| Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr |     |     |      |
| 345   | 350 | 355 |      |
| ttt gca act ggc aaa ata att gga cac atg ctc aaa tta aag gga gac |     |     | 1159 |
| Phe Ala Thr Gly Ile Ile Gly His Met Leu Lys Leu Lys Gly Asp     |     |     |      |
| 360   | 365 | 370 |      |
| ata gat tca aat gca gct att gat ctt agc aac aaa gct tca tta gca |     |     | 1207 |
| Ile Asp Ser Asn Ala Ala Ile Asp Leu Ser Asn Lys Ala Ser Leu Ala |     |     |      |
| 375   | 380 | 385 | 390  |
| ttc tta caa aag cat tta gga ctt cat aaa gat ttt gat cag tgg gac |     |     | 1255 |
| Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln Trp Asp |     |     |      |
| 395   | 400 | 405 |      |
| tgc ttg att gaa gga gat gat gag aat ctt att cca ggg acc aac att |     |     | 1303 |
| Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu Ile Pro Gly Thr Asn Ile |     |     |      |
| 410   | 415 | 420 |      |
| aac aca acc aat caa cac atc atg tta cag aac tct tca gga ata gag |     |     | 1351 |

Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly Ile Glu  
425 430 435

aaa tac aat t 1361  
Lys Tyr Asn  
440

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<212> PRT  
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<400> 10  
Gln Tyr Ile Asn Pro Val Ala  
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<210> 11  
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<212> PRT  
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<400> 11  
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Phe Ala Thr Gly  
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Gln Tyr Ile Asn Pro Ala Val  
1 5

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